REMARKS

Enclosed herewith in full compliance with 37 C.F.R. §§1.821-1.825 is a Second Substitute Sequence Listing to be inserted into the specification as indicated above. The Second Substitute Sequence Listing in no way introduces new matter into the specification. Also submitted herewith in full compliance with 37 C.F.R. §§1.821-1.825 is a disk copy of the Second Substitute Sequence Listing. The disk copy of the Second Substitute Sequence Listing, file "3759-0106P.ST25.TXT", is identical to the paper copy, except that it lacks formatting.

The specification has been amended to add the SEQ ID NO for the sequences in the specification. Typographical errors have also been corrected. No new matter is introduced by these amendments.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. § 1.16 or under 37 C.F.R. § 1.17; particularly, extension of time fees.

Respectfully submitted,
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Attachments:
Disk Copy of Second Substitute Sequence Listing
Paper Copy of Second Substitute Sequence Listing
Version with Markings Showing Changes Made
Copy of Notice

VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

The following paragraphs inserted on August 22, 2002 at page 7, line 9, regarding Fig. 1 to Fig. 5, only, have been amended as follows:

--BRIEF DESCRIPTION OF THE DRAWINGS:

Fig. 1 shows a map of the pUC19-GFP plasmid construction;

Fig. 2a is the DNA (SEQ ID [No.]**NO:**21) and predicted primary amino acid sequence (SEQ ID [No.]**NO:**22) of GFP;

Fig. 2b is the nucleotide sequence of GFP (SEQ ID [No.]**NO:**21);

Fig. 3 is the DNA (SEQ ID [No.]**NO:**15) and predicted amino acid sequence (SEQ ID [No.]**NO:**16) of F64L-Y66H-GFP;

Fig. 4 is the DNA (SEQ ID [No.]**NO:**17) and predicted amino acid sequence (SEQ ID [No.]**NO:**18) of F64L-GFP;

Fig. 5 is the DNA (SEQ ID [No.]**NO:**19) and predicted amino acid sequence (SEQ ID [No.]**NO:**20) of F64L-S65T-GFP;--

The paragraph beginning on page 12, line 25, has been amended as follows:

-- Briefly, total RNA, isolated from A. victoria by a standard procedure (Sambrook et al., Molecular Cloning. 2., eds. (1989) (Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New York), 7.19-7.22) was converted into cDNA by using the AMV reverse transcriptase (Promega, Madison, WI, USA) as recommended by the manufacturer. The cDNA was then PCR amplified, using PCR primers designed on the basis of a previously published GFP sequence (Prasher et al., Gene 111 (1992), 229-223;

GenBank accession No. M62653) together with the UlTmaTM polymerase (Perkin Elmer, Foster City, CA, USA). The sequences of the primers were: GFP2: TGGAATAAGCTTTATGAGTAAAGGAGAAGAACTTTT **(SEQ ID NO:1)** and GFP-1:AAGAATTCGGATCCCTTTAGTGTCAATTGGAAGTCT **(SEQ ID NO:2)** Restriction endonuclease sites inserted in the 5' (a HindIII site) and 3' (EcoRI and BamHI sites) primers facilitated the cloning of the PCR amplified GFP cDNA into a slightly modified pUC19 vector. The details of the construction are as follows: LacZ Shine-Dalgarno AGGA, immediately followed by the 5' HindIII site plus an extra T and the GFP ATG codon, giving the following DNA sequence at the lacZ-promoter GFP fusion point:~P_{Lacz}-AGGAAAGCTTTATG-GFP **(SEQ ID NO:23)**. At the 3' end of the GFP cDNA, the base pair corresponding to nucleotide 770 in the published GFP sequence (GenBank accession No. M62653) was fused to the EcoRI site of the pUC19 multiple cloning site (MCS) through a PCR generated BamHI, EcoRI linker region).